BLAST Basic Local Alignment Search Tool

-

Edit and Resubmit Save Search Strategies Formatting options Download

Protein Sequence (154 letters)

Results for: lcl|57770 None(154aa) ▼

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID
  lcl|57770
Description
  None
Molecule type
  amino acid
Query Length
  154

SEQ ID NO: 12

Database Name
  nr
Description
  All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program
  BLASTP 2.2.20+ Citation

Reference
Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.
Reference - compositional score matrix adjustment
Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.
Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Search Parameters

Program	blastp
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Threshold	11
Composition-based stats	2
Filter string	F
Genetic Code	1
Window Size	40

Database

Posted date	Jun 3, 2009 5:41 PM
Number of letters	3,072,644,098
Number of sequences	8,977,105

Entrez query   none

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.329052	0.267
K	0.141985	0.041
H	0.532528	0.14

Results Statistics

|	
Length adjustment	116
Effective length of query	38
Effective length of database	2031299918
Effective search space	77189396884
Effective search space used	77189396884

Graphic Summary
Show Conserved Domains
Putative conserved domains have been detected, click on the image below for detailed results.
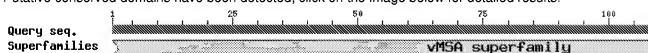
Distribution of 100 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each
alignment is indicated by one of five different colors, which divides the range of scores into five groups.
Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit
sequence causes the definition and score to be shown in the window at the top, clicking on a hit
sequence takes the user to the associated alignments. New: This graphic is an overview of database
sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score
ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing
over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment
displays the alignment detail.
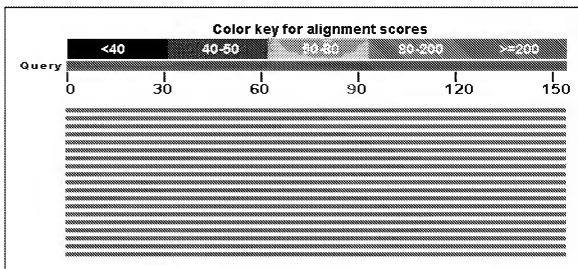
Descriptions

```
                                                                    Score      E
Sequences producing significant alignments:                        (Bits)    Value

gb|AAN37932.1|  pre-S/S protein [Hepatitis B virus]                  253     3e-66
gb|AEX60516.1|  large S protein [Hepatitis B virus]                  253     3e-66
gb|AAZ23006.1|  large S protein [Hepatitis B virus]                  253     4e-66
gb|AAC56025.2|  large surface antigen [Hepatitis B virus]            253     5e-66
gb|AAK97200.1|AF297624_4  large/middle/small S proteins [Hepat...    253     5e-66
gb|AAZ23008.1|  large S protein [Hepatitis B virus]                  253     5e-66
dbj|BAD01280.1|  LHBs [HBV genotype A]                               253     5e-66
emb|CAF29873.2|  preS1/preS2/S surface protein [Hepatitis B vi...    253     5e-66
gb|ACW86099.1|  large S protein [Hepatitis B virus]                  253     5e-66
sp|P03141.3|HBSAG_HBVA3  RecName: Full=Large envelope protein;...    253     5e-66
gb|BAF48757.1|  envelope protein [Hepatitis B virus]                 253     5e-66
gb|ABR04415.1|  large surface protein [Hepatitis B virus]            253     5e-66
dbj|BAG66757.1|  PreS1-S protein [Hepatitis B virus]                 253     6e-66
dbj|BAD02316.1|  large surface protein [Hepatitis B virus]           253     6e-66
emb|CAC51294.1|  large surface antigen [Hepatitis B virus]           253     6e-66
gb|ACF95017.1|  large S protein [Hepatitis B virus]                  253     6e-66
dbj|BAF81672.1|  preS/S protein [Hepatitis B virus]                  253     6e-66
gb|AAL68820.1|  surface antigen [Hepatitis B virus]                  253     6e-66
gb|AAR07096.1|  large S protein [Hepatitis B virus]                  252     6e-66
gb|AAZ07092.1|  large S protein [Hepatitis B virus] >gb|AAT907...    252     6e-66
gb|ACF95172.1|  large S protein [Hepatitis B virus]                  252     6e-66
gb|ACD65255.1|  large S protein [Hepatitis B virus]                  252     6e-66
gb|AAK58374.1|  PreS1+PreS2+HBsAg [synthetic construct] >gb|AA...    252     6e-66
gb|AAX07610.1|  pre-S1 protein [Hepatitis B virus]                   252     6e-66
gb|AAR07698.1|  large S protein [Hepatitis B virus]                  252     6e-66
dbj|BAF61676.1|  preS/S protein [Hepatitis B virus]                  252     6e-66
dbj|BAE92978.1|  large S protein [Hepatitis B virus]                 252     6e-66
gb|AAB47467.1|  large S protein                                      252     6e-66
gb|ACF95003.1|  large S protein [Hepatitis B virus]                  252     6e-66
gb|ACF95193.1|  large S protein [Hepatitis B virus]                  252     6e-66
emb|CAA84792.1|  surface protein S [Hepatitis B virus]               252     6e-66
gb|AAB47466.1|  large S protein                                      252     6e-66
gb|ABQ43830.1|  large S protein [Hepatitis B virus]                  252     6e-66
gb|ACD65255.1|  large S protein [Hepatitis B virus]                  252     6e-66
gb|AAB47468.1|  large S protein                                      252     7e-66
gb|AAD40215.1|AF090841_4  PreS1+PreS2+HBsAg [Hepatitis B virus]      252     7e-66
emb|CAL29861.1|  large surface antigen [Hepatitis B virus]           252     8e-66
gb|AAG37846.1|  pre-S/S protein [Hepatitis B virus]                  252     8e-66
gb|AAK97196.1|AF297623_4  large/middle/small S proteins [Hepat...    252     8e-66
gb|ABG43898.1|  large S protein [Hepatitis B virus]                  252     8e-66
gb|AAY25271.1|  large S protein [Hepatitis B virus]                  252     8e-66
gb|ACR81323.1|  large S protein [Hepatitis B virus]                  252     8e-66
gb|ABQ43374.1|  large S protein [Hepatitis B virus] >gb|ABQ438...    252     9e-66
gb|AAA45528.1|  B1 wild-type molecule; ORF1 [Hepatitis B virus]      252     9e-66
emb|CAQ86627.1|  large S protein [Hepatitis B virus]                 252     9e-66
emb|CAQ86631.1|  large S protein [Hepatitis B virus]                 252     9e-66
gb|ABQ43819.1|  large S protein [Hepatitis B virus]                  252     9e-66
gb|ABQ43894.1|  large S protein [Hepatitis B virus]                  252     9e-66
gb|AAY25278.1|  large S protein [Hepatitis B virus]                  252     9e-66
gb|AAY25216.1|  large S protein [Hepatitis B virus]                  252     9e-66
gb|AEQ43924.1|  large S protein [Hepatitis B virus]                  252     1e-65
gb|AEW03058.1|  large S protein [Hepatitis B virus]                  252     1e-65
gb|ABQ43833.1|  large S protein [Hepatitis B virus]                  252     1e-65
gb|AAY25336.1|  large S protein [Hepatitis B virus]                  252     1e-65
gb|AAR07161.1|  large S protein [Hepatitis B virus]                  252     1e-65
gb|ABD37092.1|  envelope protein [Hepatitis B virus]                 252     1e-65
gb|AAK97188.1|AF297621_4  large/middle/small S proteins [Hepat...    251     1e-65
```

```
gb|AAY25237.1|    large S protein [Hepatitis B virus]              251   1e-65
gb|ABZ85698.1|    large S protein [Hepatitis B virus]              251   1e-65
gb|AAS37936.1|    pre-S2/S protein [Hepatitis B virus]             251   1e-65
gb|BAE94219.1|    Large S protein [Hepatitis B virus]              251   1e-65
gb|AAQ91933.1|    surface protein [Hepatitis B virus]              251   1e-65
emb|CAQ66617.1|   large S protein [Hepatitis B virus]              251   1e-65
gb|ACH81331.1|    large S protein [Hepatitis B virus]              251   1e-65
gb|AAP79727.1|    large S protein [Hepatitis B virus]              251   1e-65
gb|AAD40219.1|AF090843_4    PreS1+PreS2+HBsAg [Hepatitis B virus]  251   1e-65
gb|ABQ43231.1|    large S protein [Hepatitis B virus]              251   1e-65
gb|AAQ81917.1|    surface protein [Hepatitis B virus]              251   1e-65
dbj|BAG58764.1|   PreS1-S protein [Hepatitis B virus]              251   1e-65
gb|AAC59024.3|    large surface antigen [Hepatitis B virus]        251   1e-65
gb|ACF95016.1|    middle S protein [Hepatitis B virus]             251   1e-65
gb|ABQ43631.1|    middle S protein [Hepatitis B virus]             251   2e-65
gb|ABA16795.1|    middle S protein [Hepatitis B virus]             251   2e-65
gb|AAC58096.1|    middle S protein [Hepatitis B virus] >gb|AAC58...251   2e-65
gb|ABQ43899.1|    middle S protein [Hepatitis B virus]             251   2e-65
gb|AAM96927.1|    middle S protein [Hepatitis B virus]             251   2e-65
gb|ABQ43928.1|    large S protein [Hepatitis B virus]              251   2e-65
gb|ABQ43895.1|    middle S protein [Hepatitis B virus]             251   2e-65
gb|ABH04419.1|    middle surface protein [Hepatitis B virus]       251   2e-65
gb|ABQ43654.1|    large S protein [Hepatitis B virus]              251   2e-65
dbj|BAG63776.1|   PreS1-S protein [Hepatitis B virus]              251   2e-65
gb|ACI16698.1|    S protein [Hepatitis B virus]                    251   2e-65
gb|ABQ43923.1|    middle S protein [Hepatitis B virus] >gb|ACD65...251   2e-65
dbj|BAE94222.1|   Large S protein [Hepatitis B virus]              251   2e-65
gb|AAT90410.1|    large S protein [Hepatitis B virus]              250   2e-65
gb|AAG12699.1|    preS1 [Hepatitis B virus]                        250   2e-65
gb|ABQ43932.1|    middle S protein [Hepatitis B virus]             250   2e-65
gb|AAG12705.1|    preS1 [Hepatitis B virus]                        250   3e-65
gb|ACE77880.1|    middle S protein [Hepatitis B virus]             250   3e-65
gb|ABI15463.1|    pre-S2 protein [Hepatitis B virus] >gb|ABI1549...250   3e-65
gb|ABO41307.1|    S protein [Hepatitis B virus]                    250   3e-65
gb|ABM90718.1|    HBsAg [Hepatitis B virus]                        250   3e-65
gb|AAO12693.1|    preS1 [Hepatitis B virus]                        250   3e-65
gb|ABQ43887.1|    middle S protein [Hepatitis B virus]             250   3e-65
gb|ABI15529.1|    pre-S2 protein [Hepatitis B virus]               250   3e-65
gb|ABO41295.1|    S protein [Hepatitis B virus] >gb|ABO41296.1| ...250   3e-65
gb|ABM90729.1|    HBsAg [Hepatitis B virus]                        250   3e-65
gb|ABO41267.1|    S protein [Hepatitis B virus] >gb|ABO41268.1| ...250   4e-65
gb|ABI15533.1|    pre-S2 protein [Hepatitis B virus]               250   4e-65
```

Alignments Select All Get selected sequences Distance tree of results Multiple alignment

```
>gb|AAD37942.1|  pre-S/S protein [Hepatitis B virus]
Length=387

 Score =  253 bits (647),  Expect = 3e-66, Method: Compositional matrix adjust.
 Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

Query  1    GGSPVCLGQNSQSPTSNHSPTSCPPICPGYRWMCLRRFIIFLFILLLCLIFLLVLLDYQG  60
Sbjct  215  ...........................................................  274

Query  61   MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAKYL  120
Sbjct  275  ...........T....P...........................S........  334

Query  121  WVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW  154
Sbjct  335  .E.................Q..........  368


>gb|ABX60516.1|  large S protein [Hepatitis B virus]
Length=383
```

```
  Score = 253 bits (647),  Expect = 3e-66, Method: Compositional matrix adjust.
  Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

Query   1    GGSPVCLGQNSQSPTSNHSPTSCPPICPGYRWMCLRRFIIFLFILLLCLIFLLVLLDYQG    60
Sbjct   217  ..............................................................    276

Query   61   MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAKYL    120
Sbjct   277  ............T....P...........................S........    336

Query   121  WVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW    154
Sbjct   337  .E...............Q..............    370
```

>gb|AAZ23006.1| large S protein [Hepatitis B virus]
Length=398

```
  Score = 253 bits (646),  Expect = 4e-66, Method: Compositional matrix adjust.
  Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

Query   1    GGSPVCLGQNSQSPTSNHSPTSCPPICPGYRWMCLRRFIIFLFILLLCLIFLLVLLDYQG    60
Sbjct   215  ..............................................................    274

Query   61   MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAKYL    120
Sbjct   275  ............T....P...........................S........    334

Query   121  WVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW    154
Sbjct   335  .E...............Q..............    368
```

>gb|AAC58025.2| large surface antigen [Hepatitis B virus]
Length=389

```
  Score = 253 bits (645),  Expect = 5e-66, Method: Compositional matrix adjust.
  Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

Query   1    GGSPVCLGQNSQSPTSNHSPTSCPPICPGYRWMCLRRFIIFLFILLLCLIFLLVLLDYQG    60
Sbjct   206  ..............................................................    265

Query   61   MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAKYL    120
Sbjct   266  ............T....P...........................S........    325

Query   121  WVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW    154
Sbjct   326  .E...............Q..............    359
```

>gb|AAK97200.1|AF297624_4 large/middle/small S proteins [Hepatitis B virus]
Length=389

```
  Score = 253 bits (645),  Expect = 5e-66, Method: Compositional matrix adjust.
  Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

Query   1    GGSPVCLGQNSQSPTSNHSPTSCPPICPGYRWMCLRRFIIFLFILLLCLIFLLVLLDYQG    60
Sbjct   206  ..............................................................    265

Query   61   MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAKYL    120
Sbjct   266  ............T....P...........................S........    325

Query   121  WVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW    154
Sbjct   326  .E...............Q..............    359
```

>gb|AAZ23008.1| large S protein [Hepatitis B virus]
Length=398

```
  Score = 253 bits (645),  Expect = 5e-66, Method: Compositional matrix adjust.
  Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

Query   1    GGSPVCLGQNSQSPTSNHSPTSCPPICPGYRWMCLRRFIIFLFILLLCLIFLLVLLDYQG    60
Sbjct   215  ..............................................................    274

Query   61   MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAKYL    120
Sbjct   275  ............T....P...........................S........    334

Query   121  WVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW    154
Sbjct   335  .E...............Q..............    368
```

>dbj|BAD91280.1| LHBs [HBV genotype A]
Length=400

```
  Score = 253 bits (645),  Expect = 5e-66, Method: Compositional matrix adjust.
  Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

Query   1   GGSPVCLGQNSQSPTSNHSPTSCPPICPGYRWMCLRRFIIFLFILLLCLIFLLVLLDYQG   60
Sbjct  217   ............................................................   276

Query  61   MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAKYL  120
Sbjct  277   ...............T....P................................S.......  336

Query 121   WVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW  154
Sbjct  337   .E................Q.........         370
```

>emb|CAF28873.2| preS1/preS2/S surface protein [Hepatitis B virus]
Length=396

```
  Score = 253 bits (645),  Expect = 5e-66, Method: Compositional matrix adjust.
  Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

Query   1   GGSPVCLGQNSQSPTSNHSPTSCPPICPGYRWMCLRRFIIFLFILLLCLIFLLVLLDYQG   60
Sbjct  213   ............................................................   272

Query  61   MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAKYL  120
Sbjct  273   ...............T....P................................S.......  332

Query 121   WVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW  154
Sbjct  333   .E................Q.........         366
```

>gb|ACH86089.1| large S protein [Hepatitis B virus]
Length=390

```
  Score = 253 bits (645),  Expect = 5e-66, Method: Compositional matrix adjust.
  Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

Query   1   GGSPVCLGQNSQSPTSNHSPTSCPPICPGYRWMCLRRFIIFLFILLLCLIFLLVLLDYQG   60
Sbjct  217   ............................................................   276

Query  61   MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAKYL  120
Sbjct  277   ...............T....P................................S.......  336

Query 121   WVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW  154
Sbjct  337   .E................Q.........         370
```

>sp|P03141.3|HBSAG_HBVA3 RecName: Full=Large envelope protein; AltName: Full=Lar
protein; AltName: Full=L glycoprotein; AltName: Full=Major
surface antigen; AltName: Full=Large S protein; AltName:
Full=L-HBsAg; Short=LHB
 emb|CAA26539.1| unnamed protein product [Hepatitis B virus]
Length=400

```
  Score = 253 bits (645),  Expect = 5e-66, Method: Compositional matrix adjust.
  Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

Query   1   GGSPVCLGQNSQSPTSNHSPTSCPPICPGYRWMCLRRFIIFLFILLLCLIFLLVLLDYQG   60
Sbjct  217   ............................................................   276

Query  61   MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAKYL  120
Sbjct  277   ...............T....P................................S.......  336

Query 121   WVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW  154
Sbjct  337   .E................Q.........         370
```

>dbj|BAF48757.1| envelope protein [Hepatitis B virus]
Length=400

```
  Score = 253 bits (645),  Expect = 5e-66, Method: Compositional matrix adjust.
  Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

Query   1   GGSPVCLGQNSQSPTSNHSPTSCPPICPGYRWMCLRRFIIFLFILLLCLIFLLVLLDYQG   60
Sbjct  217   ............................................................   276

Query  61   MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAKYL  120
Sbjct  277   ...............T....P................................S.......  336

Query 121   WVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW  154
Sbjct  337   .E................Q.........         370
```

```
>gb|ABH04415.1|  large surface protein [Hepatitis B virus]
Length=398

 Score =  253 bits (645),  Expect = 5e-66, Method: Compositional matrix adjust.
 Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

Query  1    GGSPVCLGQNSQSPTSNHSPTSCPPICPGYRWMCLRRFIIFLFILLLCLIFLLVLLDYQG  60
Sbjct  215  ............................................................  274

Query  61   MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAKYL  120
Sbjct  275  .............T....P.................................S........  334

Query  121  WVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW  154
Sbjct  335  .E................Q...............  368


>dbj|BAG68757.1|  PreS1-S protein [Hepatitis B virus]
Length=400

 Score =  253 bits (645),  Expect = 6e-66, Method: Compositional matrix adjust.
 Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

Query  1    GGSPVCLGQNSQSPTSNHSPTSCPPICPGYRWMCLRRFIIFLFILLLCLIFLLVLLDYQG  60
Sbjct  217  ............................................................  276

Query  61   MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAKYL  120
Sbjct  277  .............T....P.................................S........  336

Query  121  WVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW  154
Sbjct  337  .E................Q...............  370


>dbj|BAD02316.1|  large surface protein [Hepatitis B virus]
Length=400

 Score =  253 bits (645),  Expect = 6e-66, Method: Compositional matrix adjust.
 Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

Query  1    GGSPVCLGQNSQSPTSNHSPTSCPPICPGYRWMCLRRFIIFLFILLLCLIFLLVLLDYQG  60
Sbjct  217  ............................................................  276

Query  61   MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAKYL  120
Sbjct  277  .............T....P.................................S........  336

Query  121  WVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW  154
Sbjct  337  .E................Q...............  370


>emb|CAC51294.1|  large surface antigen [Hepatitis B virus]
Length=400

 Score =  253 bits (645),  Expect = 6e-66, Method: Compositional matrix adjust.
 Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

Query  1    GGSPVCLGQNSQSPTSNHSPTSCPPICPGYRWMCLRRFIIFLFILLLCLIFLLVLLDYQG  60
Sbjct  217  ............................................................  276

Query  61   MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAKYL  120
Sbjct  277  .............T....P.................................S........  336

Query  121  WVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW  154
Sbjct  337  .E................Q...............  370


>gb|ACF95017.1|  large S protein [Hepatitis B virus]
Length=400

 Score =  253 bits (645),  Expect = 6e-66, Method: Compositional matrix adjust.
 Identities = 149/154 (96%), Positives = 150/154 (97%), Gaps = 0/154 (0%)

Query  1    GGSPVCLGQNSQSPTSNHSPTSCPPICPGYRWMCLRRFIIFLFILLLCLIFLLVLLDYQG  60
Sbjct  217  ............................................................  276

Query  61   MLPVCPLIPGSTRTSTGQCKTCTTPAQGNSMFPSCCCTKPTDGNCTCIPIPLSWAFAKYL  120
Sbjct  277  .............T....P.................................S........  336

Query  121  WVWASVRFSWLSLLVPFVRWFVGLSPTVWLSAIW  154
Sbjct  337  .E................Q...............  370
```